

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/562,469
Source: TFWP
Date Processed by STIC: 07/07/2006

ENTERED



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RAW SEQUENCE LISTING

DATE: 07/07/2006

PATENT APPLICATION: US/10/562,469

TIME: 14:20:05

Input Set: E:\405uspc.app.txt

Output Set: N:\CRF4\07072006\J562469.raw

3 <110> APPLICANT: Masato MIYAKE
 4 Tomohiro YOSHIKAWA
 5 Jun MIYAKE
 7 <120> TITLE OF INVENTION: Digital cell
 9 <130> FILE REFERENCE: 690121.405USPC
 11 <140> CURRENT APPLICATION NUMBER: US 10/562,469
 C--> 12 <141> CURRENT FILING DATE: 2005-12-22
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/009404
 15 <151> PRIOR FILING DATE: 2004-06-25
 17 <150> PRIOR APPLICATION NUMBER: JP 2003-289469
 18 <151> PRIOR FILING DATE: 2003-08-07
 20 <150> PRIOR APPLICATION NUMBER: JP 2003-181915
 21 <151> PRIOR FILING DATE: 2003-06-25
 23 <160> NUMBER OF SEQ ID NOS: 50
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1929
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)..(1929)
 35 <223> OTHER INFORMATION: fibronectin 1
 38 <400> SEQUENCE: 1
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 40 Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Ala Val Gln Cys
 41 1 5 10 15
 43 ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag 96
 44 Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln
 45 20 25 30
 47 gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc 144
 48 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser
 49 35 40 45
 51 aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa cag 192
 52 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln
 53 50 55 60
 55 tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat gga 240
 56 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly
 57 65 70 75 80
 59 gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act 288
 60 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr
 61 85 90 95
 63 tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act tat 336

CP976

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64	Cys	Phe	Asp	Lys	Tyr	Thr	Gly	Asn	Thr	Tyr	Arg	Val	Gly	Asp	Thr	Tyr	
65				100					105					110			
67	gag	cgt	cct	aaa	gac	tcc	atg	atc	tgg	gac	tgt	acc	tgc	atc	ggg	gct	384
68	Glu	Arg	Pro	Lys	Asp	Ser	Met	Ile	Trp	Asp	Cys	Thr	Cys	Ile	Gly	Ala	
69			115					120					125				
71	ggg	cga	ggg	aga	ata	agc	tgt	acc	atc	gca	aac	cgc	tgc	cat	gaa	ggg	432
72	Gly	Arg	Gly	Arg	Ile	Ser	Cys	Thr	Ile	Ala	Asn	Arg	Cys	His	Glu	Gly	
73		130					135					140					
75	ggt	cag	tcc	tac	aag	att	ggt	gac	acc	tgg	agg	aga	cca	cat	gag	act	480
76	Gly	Gln	Ser	Tyr	Lys	Ile	Gly	Asp	Thr	Trp	Arg	Arg	Pro	His	Glu	Thr	
77	145					150				155					160		
79	ggt	ggt	tac	atg	tta	gag	tgt	gtg	tgt	ctt	ggt	aat	gga	aaa	gga	gaa	528
80	Gly	Gly	Tyr	Met	Leu	Glu	Cys	Val	Cys	Leu	Gly	Asn	Gly	Lys	Gly	Glu	
81				165					170				175				
83	tgg	acc	tgc	aag	ccc	ata	gct	gag	aag	tgt	ttt	gat	cat	gct	gct	ggg	576
84	Trp	Thr	Cys	Lys	Pro	Ile	Ala	Glu	Lys	Cys	Phe	Asp	His	Ala	Ala	Gly	
85			180						185				190				
87	act	tcc	tat	gtg	gtc	gga	gaa	acg	tgg	gag	aag	ccc	tac	caa	ggc	tgg	624
88	Thr	Ser	Tyr	Val	Val	Gly	Glu	Thr	Trp	Glu	Lys	Pro	Tyr	Gln	Gly	Trp	
89			195					200				205					
91	atg	atg	gta	gat	tgt	act	tgc	ctg	gga	gaa	ggc	agc	gga	cgc	atc	act	672
92	Met	Met	Val	Asp	Cys	Thr	Cys	Leu	Gly	Glu	Gly	Ser	Gly	Arg	Ile	Thr	
93		210					215					220					
95	tgc	act	tct	aga	aat	aga	tgc	aac	gat	cag	gac	aca	agg	aca	tcc	tat	720
96	Cys	Thr	Ser	Arg	Asn	Arg	Cys	Asn	Asp	Gln	Asp	Thr	Arg	Thr	Ser	Tyr	
97	225					230				235			240				
99	aga	att	gga	gac	acc	tgg	agc	aag	aag	gat	aat	cga	gga	aac	ctg	ctc	768
100	Arg	Ile	Gly	Asp	Thr	Trp	Ser	Lys	Lys	Asp	Asn	Arg	Gly	Asn	Leu	Leu	
101				245					250				255				
103	cag	tgc	atc	tgc	aca	ggc	aac	ggc	cga	gga	gag	tgg	aag	tgt	gag	agg	816
104	Gln	Cys	Ile	Cys	Thr	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Lys	Cys	Glu	Arg	
105			260					265				270					
107	cac	acc	tct	gtg	cag	acc	aca	tcg	agc	gga	tct	ggc	ccc	ttc	acc	gat	864
108	His	Thr	Ser	Val	Gln	Thr	Thr	Ser	Gly	Ser	Gly	Pro	Phe	Thr	Asp		
109			275					280				285					
111	gtt	cgt	gca	gct	gtt	tac	caa	ccg	cag	cct	cac	ccc	cag	cct	cct	ccc	912
112	Val	Arg	Ala	Ala	Val	Tyr	Gln	Pro	Gln	Pro	His	Pro	Gln	Pro	Pro	Pro	
113		290					295					300					
115	tat	ggc	cac	tgt	gtc	aca	gac	agt	ggt	gtg	gtc	tac	tct	gtg	ggg	atg	960
116	Tyr	Gly	His	Cys	Val	Thr	Asp	Ser	Gly	Val	Val	Tyr	Ser	Val	Gly	Met	
117	305					310				315			320				
119	cag	tgg	ctg	aag	aca	caa	gga	aat	aag	caa	atg	ctt	tgc	acg	tgc	ctg	1008
120	Gln	Trp	Leu	Lys	Thr	Gln	Gly	Asn	Lys	Gln	Met	Leu	Cys	Thr	Cys	Leu	
121				325					330				335				
123	ggc	aac	gga	gtc	agc	tgc	caa	gag	aca	gct	gta	acc	cag	act	tac	ggt	1056
124	Gly	Asn	Gly	Val	Ser	Cys	Gln	Glu	Thr	Ala	Val	Thr	Gln	Thr	Tyr	Gly	
125			340					345				350					
127	ggc	aac	tca	aat	gga	gag	cca	tgt	gtc	tta	cca	ttc	acc	tac	aat	ggc	1104
128	Gly	Asn	Ser	Asn	Gly	Glu	Pro	Cys	Val	Leu	Pro	Phe	Thr	Tyr	Asn	Gly	

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129	355	360	365	
131	agg acg gac agc aca act tcg aat tat gag cag gac cag aaa tac tct	1152		
132	Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser			
133	370 375 380			
135	ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc	1200		
136	Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser			
137	385 390 395 400			
139	aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac	1248		
140	Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr			
141	405 410 415			
143	act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg	1296		
144	Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly			
145	420 425 430			
147	acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg	1344		
148	Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met			
149	435 440 445			
151	gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc	1392		
152	Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg			
153	450 455 460			
155	att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg	1440		
156	Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg			
157	465 470 475 480			
159	tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac	1488		
160	Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr			
161	485 490 495			
163	tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg	1536		
164	Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val			
165	500 505 510			
167	aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt	1584		
168	Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys			
169	515 520 525			
171	aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac	1632		
172	Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp			
173	530 535 540			
175	caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca	1680		
176	Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser			
177	545 550 555 560			
179	tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc	1728		
180	Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly			
181	565 570 575			
183	cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc	1776		
184	Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser			
185	580 585 590			
187	tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc	1824		
188	Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro			
189	595 600 605			
191	aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc	1872		
192	Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser			
193	610 615 620			

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195 aag tac att ctc agg tgg aga cct gtg agt atc cca ccc aga aac ctt      1920
196 Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu
197 625                      630                      635                      640
199 gga tac tga
200 Gly Tyr
204 <210> SEQ ID NO: 2
205 <211> LENGTH: 642
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 2
211 Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys
212 1                      5                      10                      15
215 Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln
216                      20                      25                      30
219 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser
220                      35                      40                      45
223 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln
224 50                      55                      60
227 Trp Gly Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly
228 65                      70                      75                      80
231 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr
232                      85                      90                      95
235 Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr
236                      100                     105                     110
239 Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala
240                      115                     120                     125
243 Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly
244                      130                     135                     140
247 Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr
248 145                     150                     155                     160
252 Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu
253                      165                     170                     175
256 Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly
257                      180                     185                     190
260 Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp
261                      195                     200                     205
264 Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr
265                      210                     215                     220
268 Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr
269 225                     230                     235                     240
272 Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu
273                      245                     250                     255
276 Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg
277                      260                     265                     270
280 His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp
281                      275                     280                     285
284 Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro
285                      290                     295                     300
288 Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met

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289 305          310          315          320
292 Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu
293          325          330          335
296 Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly
297          340          345          350
300 Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly
301          355          360          365
304 Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser
305          370          375          380
308 Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
309 385          390          395          400
312 Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr
313          405          410          415
316 Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly
317          420          425          430
320 Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met
321          435          440          445
324 Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
325          450          455          460
328 Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
329 465          470          475          480
332 Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
333          485          490          495
336 Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val
337          500          505          510
340 Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys
341          515          520          525
344 Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp
345          530          535          540
348 Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
349 545          550          555          560
352 Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
353          565          570          575
356 Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
357          580          585          590
360 Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
361          595          600          605
364 Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
365          610          615          620
368 Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu
369 625          630          635          640
372 Gly Tyr
376 <210> SEQ ID NO: 3
377 <211> LENGTH: 1437
378 <212> TYPE: DNA
379 <213> ORGANISM: Mus musculus
381 <220> FEATURE:
382 <221> NAME/KEY: CDS
383 <222> LOCATION: (1) .. (1437)

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/562,469

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 99
Seq#:31; N Pos. 13
Seq#:33; N Pos. 15
Seq#:35; N Pos. 108
Seq#:37; N Pos. 940,1083
Seq#:37; Xaa Pos. 286
Seq#:38; Xaa Pos. 286

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:12; Line(s) 4237

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:12,47,48

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:4240 M:112 C: (48) String data converted to lower case,
L:4661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:60
L:5958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:6177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:6380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:60
L:6672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:929
L:6673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:977
L:6684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:1080
L:6767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:272